



SEQUENCE LISTING

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<120> Human E3 Alpha Ubiquitin Ligase Family

<130> 01017/35966A

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<211> 6308

<212> DNA

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<220>

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ttc Phe 1630	tgt Cys 1630	ggg Gly 1630	gct Ala 1630	ata Ile 1630	cta Leu 1630	tgt Cys 1635	tct Ser 1635	cag Gln 1635	aac Asn 1635	att Ile 1640	tgc Cys 1640	tgc Cys 1640	cag Gln 1640	gaa Glu 1640	5624
att Ile 1645	gtg Val 1645	aac Asn 1645	ggg Gly 1645	gaa Glu 1645	gag Glu 1645	gtt Val 1650	gga Gly 1650	gct Ala 1650	tgc Cys 1650	att Ile 1655	ttt Phe 1655	cac His 1655	gca Ala 1655	ctt Leu 1655	5669
cac His 1660	tgt Cys 1660	gga Gly 1660	gcc Ala 1660	gga Gly 1660	gtc Val 1660	tgc Cys 1665	att Ile 1665	ttc Phe 1665	cta Leu 1665	aaa Lys 1670	atc Ile 1670	aga Arg 1670	gaa Glu 1670	tgc Cys 1670	5714

cga gtg gtc ctg gtt gaa ggt aaa gcc aga ggc tgt gcc tat cca 5759
 Arg Val Val Leu Val Glu Gly Lys Ala Arg Gly Cys Ala Tyr Pro
 1675 1680 1685

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 Ala Pro Tyr Leu Asp Glu Tyr Gly Glu Thr Asp Pro Gly Leu Lys
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 Arg Gly Asn Pro Leu His Leu Ser Arg Glu Arg Tyr Arg Lys Leu
 1705 1710 1715

cat ttg gtc tgg caa caa cac tgc att ata gaa gag att gct agg 5894
 His Leu Val Trp Gln Gln His Cys Ile Ile Glu Glu Ile Ala Arg
 1720 1725 1730

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 Ser Gln Glu Thr Asn Gln Met Leu Phe Gly Phe Asn Trp Gln Leu
 1735 1740 1745

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 Leu

gctgattcaa aattatggaa aacttttctga gggctgggaa agtattggag ggtcttttgc 6052

tccatgtcca gggttactta catcaataaa atatttctta atggagtatt gctttcaatt 6112

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 35 40 45
 Glu Ile Tyr Phe Ala Glu Met Asp Pro Asp Leu Glu Lys Gln Glu Glu
 50 55 60
 Ser Val Gln Met Ser Ile Phe Thr Pro Leu Glu Trp Tyr Leu Phe Gly
 65 70 75 80
 Glu Asp Pro Asp Ile Cys Leu Glu Lys Leu Lys His Ser Gly Ala Phe
 85 90 95
 Gln Leu Cys Gly Arg Val Phe Lys Ser Gly Glu Thr Thr Tyr Ser Cys
 100 105 110

130

A

Arg	Asp	Cys	Ala	Ile	Asp	Pro	Thr	Cys	Val	Leu	Cys	Met	Asp	Cys	Phe	115	120	125
Gln	Asp	Ser	Val	His	Lys	Asn	His	Arg	Tyr	Lys	Met	His	Thr	Ser	Thr	130	135	140
Gly	Gly	Gly	Phe	Cys	Asp	Cys	Gly	Asp	Thr	Glu	Ala	Trp	Lys	Thr	Gly	145	150	155
Pro	Phe	Cys	Val	Asn	His	Glu	Pro	Gly	Arg	Ala	Gly	Thr	Ile	Lys	Glu	165	170	175
Asn	Ser	Arg	Cys	Pro	Leu	Asn	Glu	Glu	Val	Ile	Val	Gln	Ala	Arg	Lys	180	185	190
Ile	Phe	Pro	Ser	Val	Ile	Lys	Tyr	Val	Val	Glu	Met	Thr	Ile	Trp	Glu	195	200	205
Glu	Glu	Lys	Glu	Leu	Pro	Pro	Glu	Leu	Gln	Ile	Arg	Glu	Lys	Asn	Glu	210	215	220
Arg	Tyr	Tyr	Cys	Val	Leu	Phe	Asn	Asp	Glu	His	His	Ser	Tyr	Asp	His	225	230	235
Val	Ile	Tyr	Ser	Leu	Gln	Arg	Ala	Leu	Asp	Cys	Glu	Leu	Ala	Glu	Ala	245	250	255
Gln	Leu	His	Thr	Thr	Ala	Ile	Asp	Lys	Glu	Gly	Arg	Arg	Ala	Val	Lys	260	265	270
Ala	Gly	Ala	Tyr	Ala	Ala	Cys	Gln	Glu	Ala	Lys	Glu	Asp	Ile	Lys	Ser	275	280	285
His	Ser	Glu	Asn	Val	Ser	Gln	His	Pro	Leu	His	Val	Glu	Val	Leu	His	290	295	300
Ser	Glu	Ile	Met	Ala	His	Gln	Lys	Phe	Ala	Leu	Arg	Leu	Gly	Ser	Trp	305	310	315
Met	Asn	Lys	Ile	Met	Ser	Tyr	Ser	Ser	Asp	Phe	Arg	Gln	Ile	Phe	Cys	325	330	335
Gln	Ala	Cys	Leu	Arg	Glu	Glu	Pro	Asp	Ser	Glu	Asn	Pro	Cys	Leu	Ile	340	345	350
Ser	Arg	Leu	Met	Leu	Trp	Asp	Ala	Lys	Leu	Tyr	Lys	Gly	Ala	Arg	Lys	355	360	365
Ile	Leu	His	Glu	Leu	Ile	Phe	Ser	Ser	Phe	Phe	Met	Glu	Met	Glu	Tyr	370	375	380
Lys	Lys	Leu	Phe	Ala	Met	Glu	Phe	Val	Lys	Tyr	Tyr	Lys	Gln	Leu	Gln	385	390	395
Lys	Glu	Tyr	Ile	Ser	Asp	Asp	His	Asp	Arg	Ser	Ile	Ser	Ile	Thr	Ala	405	410	415
Leu	Ser	Val	Gln	Met	Phe	Thr	Val	Pro	Thr	Leu	Ala	Arg	His	Leu	Ile	420	425	430
Glu	Glu	Gln	Asn	Val	Ile	Ser	Val	Ile	Thr	Glu	Thr	Leu	Leu	Glu	Val	435	440	445

Met Arg Glu Ile Ile His Leu Leu Cys Ile Glu Pro Met Pro His Ser
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 Ala Ile Ala Lys Asn Leu Pro Glu Asn Glu Asn Asn Glu Thr Gly Leu
 785 790 795 800
 Glu Asn Val Ile Asn Lys Val Ala Thr Phe Lys Lys Pro Gly Val Ser
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 Gly His Gly Val Tyr Glu Leu Lys Asp Glu Ser Leu Lys Asp Phe Asn
 820 825 830
 Met Tyr Phe Tyr His Tyr Ser Lys Thr Gln His Ser Lys Ala Glu His
 835 840 845
 Met Gln Lys Lys Arg Arg Lys Gln Glu Asn Lys Asp Glu Ala Leu Pro
 850 855 860
 Pro Pro Pro Pro Pro Glu Phe Cys Pro Ala Phe Ser Lys Val Ile Asn
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 Trp Ile Leu Gln Met Phe Asp Thr Val Lys Arg Leu Arg Glu Lys Ser
 980 985 990
 Cys Leu Ile Val Ala Thr Thr Ser Gly Ser Glu Ser Ile Lys Asn Asp
 995 1000 1005
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 Cys Asn Thr Val Ile Pro Ile Ile Pro Leu Gln Pro Gln Lys Ile
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 Asn Ser Glu Asn Ala Asp Ala Leu Ala Gln Leu Leu Thr Leu Ala
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 Arg His Ala Lys Gly Glu Asn Pro Ile Pro Ile Phe Phe Asn Gln
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 Gly Met Gly Asp Ser Thr Leu Glu Phe His Ser Ile Leu Ser Phe
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 1370 1375 1380
 Val Val Leu Pro Asn Ile Lys Ser Glu Asp Thr Pro Cys Leu Leu
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 Ser Ile Asp Leu Phe His Val Leu Val Gly Ala Val Leu Ala Phe
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Val	Ser	Ser	Ser	Tyr	Asn	His	Leu	Tyr	Leu	Phe	His	Leu	Ile	Thr
1430						1435					1440			
Met	Ala	His	Met	Leu	Gln	Ile	Leu	Leu	Thr	Val	Asp	Thr	Gly	Leu
1445						1450					1455			
Pro	Leu	Ala	Gln	Val	Gln	Glu	Asp	Ser	Glu	Glu	Ala	His	Ser	Ala
1460						1465					1470			
Ser	Ser	Phe	Phe	Ala	Glu	Ile	Ser	Gln	Tyr	Thr	Ser	Gly	Ser	Ile
1475						1480					1485			
Gly	Cys	Asp	Ile	Pro	Gly	Trp	Tyr	Leu	Trp	Val	Ser	Leu	Lys	Asn
1490						1495					1500			
Gly	Ile	Thr	Pro	Tyr	Leu	Arg	Cys	Ala	Ala	Leu	Phe	Phe	His	Tyr
1505						1510					1515			
Leu	Leu	Gly	Val	Thr	Pro	Pro	Glu	Glu	Leu	His	Thr	Asn	Ser	Ala
1520						1525					1530			
Glu	Gly	Glu	Tyr	Ser	Ala	Leu	Cys	Ser	Tyr	Leu	Ser	Leu	Pro	Thr
1535						1540					1545			
Asn	Leu	Phe	Leu	Leu	Phe	Gln	Glu	Tyr	Trp	Asp	Thr	Val	Arg	Pro
1550						1555					1560			
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1595						1600					1605			
Ser	His	Phe	Arg	Cys	Pro	Arg	Ser	Ala	Asp	Asp	Glu	Arg	Lys	His
1610						1615					1620			
Pro	Val	Leu	Cys	Leu	Phe	Cys	Gly	Ala	Ile	Leu	Cys	Ser	Gln	Asn
1625						1630					1635			
Ile	Cys	Cys	Gln	Glu	Ile	Val	Asn	Gly	Glu	Glu	Val	Gly	Ala	Cys
1640						1645					1650			
Ile	Phe	His	Ala	Leu	His	Cys	Gly	Ala	Gly	Val	Cys	Ile	Phe	Leu
1655						1660					1665			
Lys	Ile	Arg	Glu	Cys	Arg	Val	Val	Leu	Val	Glu	Gly	Lys	Ala	Arg
1670						1675					1680			
Gly	Cys	Ala	Tyr	Pro	Ala	Pro	Tyr	Leu	Asp	Glu	Tyr	Gly	Glu	Thr
1685						1690					1695			
Asp	Pro	Gly	Leu	Lys	Arg	Gly	Asn	Pro	Leu	His	Leu	Ser	Arg	Glu
1700						1705					1710			

Arg Tyr Arg Lys Leu His Leu Val Trp Gln Gln His Cys Ile Ile
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tccttccttt ccggttcacg tcacccttct ctccctctgt tgctccacct gcagccactt 180
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Met
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Ala Ser Glu Leu Glu Pro Glu Val Gln Ala Ile Asp Arg Ser Leu Leu
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gaa tgt tcg gcc gag gag att gcg ggg aaa tgg ctg caa gca act gac 393
Glu Cys Ser Ala Glu Glu Ile Ala Gly Lys Trp Leu Gln Ala Thr Asp
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ctc act aga gaa gtg tac cag cat tta gcc cac tat gta ccc aaa atc 441
Leu Thr Arg Glu Val Tyr Gln His Leu Ala His Tyr Val Pro Lys Ile
35 40 45
tac tgc agg ggt ccc aac cct ttt cca cag aaa gaa gac atg ctg gca 489
Tyr Cys Arg Gly Pro Asn Pro Phe Pro Gln Lys Glu Asp Met Leu Ala
50 55 60 65
cag cat gtt ttg ttg gga cca atg gaa tgg tac ctt tgt ggt gaa gat 537
Gln His Val Leu Leu Gly Pro Met Glu Trp Tyr Leu Cys Gly Glu Asp
70 75 80
cct gca ttt gga ttt cca aaa ctt gag caa gca aac aaa cct tct cat 585
Pro Ala Phe Gly Phe Pro Lys Leu Glu Gln Ala Asn Lys Pro Ser His
85 90 95
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Leu Cys Gly Arg Val Phe Lys Val Gly Glu Pro Thr Tyr Ser Cys Arg
100 105 110
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Asp Cys Ala Val Asp Pro Thr Cys Val Leu Cys Met Glu Cys Phe Leu
115 120 125

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Gln Asn Arg Glu Asp Thr Ala Leu Pro Pro Pro Val Leu Pro Pro Phe	
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Cys Pro Leu Phe Ala Ser Leu Val Asn Ile Leu Gln Ser Asp Val Met	
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Ala Pro Lys Asn Ser Pro Ser Ile Leu Ala Met Leu Glu Thr Leu Gln	
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Lys Thr Phe Asn Ala Val Lys Lys Met Arg Glu Ser Ser Pro Thr Ser	
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Pro Val Ala Glu Thr Glu Gly Thr Ile Met Glu Glu Ser Ser Arg	
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Ser Asp Met Thr Leu Thr Ala Leu Gly Pro Thr Gln Thr Gln Val	
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gct Ala 1520	tta Leu	ttt Phe	ttt Phe	cat His	tac Tyr	tta Leu	aat Asn	gga Gly	gtt Val	cct Pro	tcc Ser	cca Pro	ccc Pro	gac Asp	4896
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 agaaaaatta g 6300

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 Asp Leu Thr Arg Glu Val Tyr Gln His Leu Ala His Tyr Val Pro Lys
 35 40 45
 Ile Tyr Cys Arg Gly Pro Asn Pro Phe Pro Gln Lys Glu Asp Met Leu
 50 55 60
 Ala Gln His Val Leu Leu Gly Pro Met Glu Trp Tyr Leu Cys Gly Glu
 65 70 75 80
 Asp Pro Ala Phe Gly Phe Pro Lys Leu Glu Gln Ala Asn Lys Pro Ser
 85 90 95
 His Leu Cys Gly Arg Val Phe Lys Val Gly Glu Pro Thr Tyr Ser Cys
 100 105 110
 Arg Asp Cys Ala Val Asp Pro Thr Cys Val Leu Cys Met Glu Cys Phe
 115 120 125
 Leu Gly Ser Ile His Arg Asp His Arg Tyr Arg Met Thr Thr Ser Gly
 130 135 140
 Gly Gly Gly Phe Cys Asp Cys Gly Asp Thr Glu Ala Trp Lys Glu Gly
 145 150 155 160
 Pro Tyr Cys Gln Lys His Glu Leu Asn Thr Ser Glu Ile Glu Glu Glu
 165 170 175
 Glu Asp Pro Leu Val His Leu Ser Glu Asp Val Ile Ala Arg Thr Tyr
 180 185 190

Asn	Ile	Phe	Ala	Ile	Thr	Phe	Arg	Tyr	Ala	Val	Glu	Ile	Leu	Thr	Trp
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Glu	Lys	Glu	Ser	Glu	Leu	Pro	Ala	Asp	Leu	Glu	Met	Val	Glu	Lys	Ser
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Asp	Thr	Tyr	Tyr	Cys	Met	Leu	Phe	Asn	Asp	Glu	Val	His	Thr	Tyr	Glu
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Gln	Val	Ile	Tyr	Thr	Leu	Gln	Lys	Ala	Val	Asn	Cys	Thr	Gln	Lys	Glu
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Ala	Ile	Gly	Phe	Ala	Thr	Thr	Val	Asp	Arg	Asp	Gly	Arg	Arg	Ser	Val
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Leu	Gly	Ser	Ile	Ile	Gly	Tyr	Ser	Asp	Gly	Leu	Arg	Arg	Ile	Leu	Cys
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Gln	Val	Gly	Leu	Gln	Glu	Gly	Pro	Asp	Gly	Glu	Asn	Ser	Ser	Leu	Val
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Arg	Asp	Phe	Met	Glu	Asp	Asp	His	Glu	Arg	Ala	Val	Ser	Val	Thr	Ala
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Thr	Glu	Glu	Asn	Leu	Met	Ser	Ile	Ile	Ile	Lys	Thr	Phe	Met	Asp	His
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Ala	Leu	Gln	Ala	Phe	Lys	Phe	Arg	Arg	Val	Gln	Ser	Leu	Ile	Leu	Asp
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Leu	Lys	Tyr	Val	Leu	Ile	Ser	Lys	Pro	Thr	Glu	Trp	Ser	Asp	Glu	Leu
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Arg	Gln	Lys	Phe	Leu	Glu	Gly	Phe	Asp	Ala	Phe	Leu	Glu	Leu	Leu	Lys
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Cys	Met	Gln	Gly	Met	Asp	Pro	Ile	Thr	Arg	Gln	Val	Gly	Gln	His	Ile
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Thr	His	Val	Ile	Ser	Met	Met	Gln	Asp	Trp	Cys	Ala	Ser	Asp	Glu	Lys	545	550	555
Val	Leu	Ile	Glu	Ala	Tyr	Lys	Lys	Cys	Leu	Ala	Val	Leu	Met	Gln	Cys	565	570	575
His	Gly	Gly	Tyr	Thr	Asp	Gly	Glu	Gln	Pro	Ile	Thr	Leu	Ser	Ile	Cys	580	585	590
Gly	His	Ser	Val	Glu	Thr	Ile	Arg	Tyr	Cys	Val	Ser	Gln	Glu	Lys	Val	595	600	605
Ser	Ile	His	Leu	Pro	Val	Ser	Arg	Leu	Leu	Ala	Gly	Leu	His	Val	Leu	610	615	620
Leu	Ser	Lys	Ser	Glu	Val	Ala	Tyr	Lys	Phe	Pro	Glu	Leu	Leu	Pro	Leu	625	630	635
Ser	Glu	Leu	Ser	Pro	Pro	Met	Leu	Ile	Glu	His	Pro	Leu	Arg	Cys	Leu	645	650	655
Val	Leu	Cys	Ala	Gln	Val	His	Ala	Gly	Met	Trp	Arg	Arg	Asn	Gly	Phe	660	665	670
Ser	Leu	Val	Asn	Gln	Ile	Tyr	Tyr	Tyr	His	Asn	Val	Lys	Cys	Arg	Arg	675	680	685
Glu	Met	Phe	Asp	Lys	Asp	Val	Val	Met	Leu	Gln	Thr	Gly	Val	Ser	Met	690	695	700
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Tyr	Gln	Ile	Phe	Ser	Thr	Pro	Asp	Tyr	Gly	Lys	Arg	Phe	Ser	Ser	Glu	725	730	735
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Met	Leu	Tyr	Leu	Ile	Ile	Met	Leu	Val	Gly	Glu	Arg	Phe	Ser	Pro	Gly	755	760	765
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Val	Ala	His	Phe	Lys	Lys	Pro	Gly	Leu	Thr	Gly	Arg	Gly	Met	Tyr	Glu	820	825	830
Leu	Lys	Pro	Glu	Cys	Ala	Lys	Glu	Phe	Asn	Leu	Tyr	Phe	Tyr	His	Phe	835	840	845

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Tyr Leu Ser Leu Pro Asn Asn Leu Ile Cys Leu Phe Gln Glu Asn	1550	1555	1560
Ser Glu Ile Met Asn Ser Leu Ile Glu Ser Trp Cys Arg Asn Ser	1565	1570	1575
Glu Val Lys Arg Tyr Leu Glu Gly Glu Arg Asp Ala Ile Arg Tyr	1580	1585	1590
Pro Arg Glu Ser Asn Lys Leu Ile Asn Leu Pro Glu Asp Tyr Ser	1595	1600	1605
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Glu Asp Val Gly Ala Cys Thr Ala His Thr Tyr Ser Cys Gly Ser	1655	1660	1665
Gly Val Gly Ile Phe Leu Arg Val Arg Glu Cys Gln Val Leu Phe	1670	1675	1680
Leu Ala Gly Lys Thr Lys Gly Cys Phe Tyr Ser Pro Pro Tyr Leu	1685	1690	1695
Asp Asp Tyr Gly Glu Thr Asp Gln Gly Leu Arg Arg Gly Asn Pro	1700	1705	1710
Leu His Leu Cys Lys Glu Arg Phe Lys Lys Ile Gln Lys Leu Trp	1715	1720	1725
His Gln His Ser Val Thr Glu Glu Ile Gly His Ala Gln Glu Ala	1730	1735	1740
Asn Gln Thr Leu Val Gly Ile Asp Trp Gln His Leu	1745	1750	1755

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Val	Tyr	His	Gln	Leu	Phe	Met	Ser	Ser	Leu	Leu	Met	Asp	Leu	Lys	Tyr	370	375	380	
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Arg	Asp	Phe	Met	Glu	Asp	Asp	His	Glu	Arg	Ala	Val	Ser	Val	Thr	Ala	405	410	415	
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Arg	Gln	Lys	Phe	Leu	Gln	Gly	Phe	Asp	Ala	Phe	Leu	Glu	Leu	Leu	Lys	500	505	510	
Cys	Met	Gln	Gly	Met	Asp	Pro	Ile	Thr	Arg	Gln	Val	Gly	Gln	His	Ile	515	520	525	
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Leu Ser Cys Gly Thr His Thr Gly Ser Cys Gly His Val Met His
1160 1165 1170
Ala His Cys Trp Gln Arg Tyr Phe Asp Ser Val Gln Ala Lys Glu
1175 1180 1185
Gln Arg Arg Gln Gln Arg Leu Arg Leu His Thr Ser Tyr Asp Val
1190 1195 1200

Glu	Asn	Gly	Glu	Phe	Leu	Cys	Pro	Leu	Cys	Glu	Cys	Leu	Ser	Asn
1205						1210					1215			
Thr	Val	Ile	Pro	Leu	Leu	Leu	Pro	Pro	Arg	Ser	Ile	Leu	Ser	Arg
1220						1225					1230			
Arg	Leu	Asn	Phe	Ser	Asp	Gln	Pro	Asp	Leu	Ala	Gln	Trp	Thr	Arg
1235						1240					1245			
Ala	Val	Thr	Gln	Gln	Ile	Lys	Val	Val	Gln	Met	Leu	Arg	Arg	Lys
1250						1255					1260			
His	Asn	Ala	Ala	Asp	Thr	Ser	Ser	Ser	Glu	Asp	Thr	Glu	Ala	Met
1265						1270					1275			
Asn	Ile	Ile	Pro	Ile	Pro	Glu	Gly	Phe	Arg	Pro	Asp	Phe	Tyr	Pro
1280						1285					1290			
Arg	Asn	Pro	Tyr	Ser	Asp	Ser	Ile	Lys	Glu	Met	Leu	Thr	Thr	Phe
1295						1300					1305			
Gly	Thr	Ala	Ala	Tyr	Lys	Val	Gly	Leu	Lys	Val	His	Pro	Asn	Glu
1310						1315					1320			
Gly	Asp	Pro	Arg	Val	Pro	Ile	Leu	Cys	Trp	Gly	Thr	Cys	Ala	Tyr
1325						1330					1335			
Thr	Ile	Gln	Ser	Ile	Glu	Arg	Ile	Leu	Ser	Asp	Glu	Glu	Lys	Pro
1340						1345					1350			
Val	Phe	Gly	Pro	Leu	Pro	Cys	Arg	Leu	Asp	Asp	Cys	Leu	Arg	Ser
1355						1360					1365			
Leu	Thr	Arg	Phe	Ala	Ala	Ala	His	Trp	Thr	Val	Ala	Leu	Leu	Pro
1370						1375					1380			
Val	Val	Gln	Gly	His	Phe	Cys	Lys	Leu	Phe	Ala	Ser	Leu	Val	Pro
1385						1390					1395			
Ser	Asp	Ser	Tyr	Glu	Asp	Leu	Pro	Cys	Ile	Leu	Asp	Ile	Asp	Met
1400						1405					1410			
Phe	His	Leu	Leu	Val	Gly	Leu	Val	Leu	Ala	Phe	Pro	Ala	Leu	Gln
1415						1420					1425			
Cys	Gln	Asp	Phe	Ser	Gly	Ser	Ser	Leu	Ala	Thr	Gly	Asp	Leu	His
1430						1435					1440			
Ile	Phe	His	Leu	Val	Thr	Met	Ala	His	Ile	Val	Gln	Ile	Leu	Leu
1445						1450					1455			
Thr	Ser	Cys	Thr	Glu	Glu	Asn	Gly	Met	Asp	Gln	Glu	Asn	Pro	Thr
1460						1465					1470			
Gly	Glu	Glu	Glu	Leu	Ala	Ile	Leu	Ser	Leu	His	Lys	Thr	Leu	His
1475						1480					1485			
Gln	Tyr	Thr	Gly	Ser	Ala	Leu	Lys	Glu	Ala	Pro	Ser	Gly	Trp	His
1490						1495					1500			
Leu	Trp	Arg	Ser	Val	Arg	Ala	Ala	Ile	Met	Pro	Phe	Leu	Lys	Cys
1505						1510					1515			

Ser	Ala	Leu	Phe	Phe	His	Tyr	Leu	Asn	Gly	Val	Pro	Ala	Pro	Pro
1520						1525					1530			
Asp	Leu	Gln	Val	Ser	Gly	Thr	Ser	His	Phe	Glu	His	Leu	Cys	Asn
1535						1540					1545			
Tyr	Leu	Ser	Leu	Pro	Thr	Asn	Leu	Ile	His	Leu	Phe	Gln	Glu	Asn
1550						1555					1560			
Ser	Asp	Ile	Met	Asn	Ser	Leu	Ile	Glu	Ser	Trp	Cys	Gln	Asn	Ser
1565						1570					1575			
Glu	Val	Lys	Arg	Tyr	Leu	Asn	Gly	Glu	Arg	Gly	Ala	Ile	Ser	Tyr
1580						1585					1590			
Pro	Arg	Gly	Ala	Asn	Lys	Leu	Ile	Asp	Leu	Pro	Glu	Asp	Tyr	Ser
1595						1600					1605			
Ser	Leu	Ile	Asn	Gln	Ala	Ser	Asn	Phe	Ser	Cys	Pro	Lys	Ser	Gly
1610						1615					1620			
Gly	Asp	Lys	Ser	Arg	Ala	Pro	Thr	Leu	Cys	Leu	Val	Cys	Gly	Ser
1625						1630					1635			
Leu	Leu	Cys	Ser	Gln	Ser	Tyr	Cys	Cys	Gln	Ala	Glu	Leu	Glu	Gly
1640						1645					1650			
Glu	Asp	Val	Gly	Ala	Cys	Thr	Ala	His	Thr	Tyr	Ser	Cys	Gly	Ser
1655						1660					1665			
Gly	Ala	Gly	Ile	Phe	Leu	Arg	Val	Arg	Glu	Cys	Gln	Val	Leu	Phe
1670						1675					1680			
Leu	Ala	Gly	Lys	Thr	Lys	Gly	Cys	Phe	Tyr	Ser	Pro	Pro	Tyr	Leu
1685						1690					1695			
Asp	Asp	Tyr	Gly	Glu	Thr	Asp	Gln	Gly	Leu	Arg	Arg	Gly	Asn	Pro
1700						1705					1710			
Leu	His	Leu	Cys	Gln	Glu	Arg	Phe	Arg	Lys	Ile	Gln	Lys	Leu	Trp
1715						1720					1725			
Gln	Gln	His	Ser	Ile	Thr	Glu	Glu	Ile	Gly	His	Ala	Gln	Glu	Ala
1730						1735					1740			
Asn	Gln	Thr	Leu	Val	Gly	Ile	Asp	Trp	Gln	His	Leu			
1745						1750					1755			

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 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer
 -2282-91

<400> 7
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21

<210> 8
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer -
2385-35

<400> 8
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24

<210> 9
<211> 23
<212> DNA
<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Primer 2282-94

<400> 9
gtatgaactt gccgaggctt tta

23

<210> 10
<211> 23
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<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Primer 2294-37

<400> 10
caatactttc ccagccctca gaa

23

<210> 11
<211> 18
<212> DNA
<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Primer 2380-88

<400> 11
atggcgtcgc tagagcca

18

<210> 12
<211> 23
<212> DNA
<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Primer 2378-32

<400> 12
caaagcggct gagcatgac atc

23

<210> 13
 <211> 23
 <212> DNA
 <213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Primer 2381-48

<400> 13

tgaacagcca atcacactaa gca

23

<210> 14
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 <212> DNA
 <213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Primer 2385-94

<400> 14

ttataaatgc caaatgccaa

20

<210> 15
 <211> 1757
 <212> PRT
 <213> Mouse

<400> 15

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Glu Pro Pro Leu Ala Pro Gln Arg Pro Ala Ser Trp Trp Asp Gln Gln
 20 25 30

Val Asp Phe Tyr Thr Ala Phe Leu His His Leu Ala Gln Leu Val Pro
 35 40 45

Glu Ile Tyr Phe Ala Glu Met Asp Pro Asp Leu Glu Lys Gln Glu Glu
 50 55 60

Ser Val Gln Met Ser Ile Leu Thr Pro Leu Glu Trp Tyr Leu Phe Gly
 65 70 75 80

Glu Asp Pro Asp Ile Cys Leu Glu Lys Leu Lys His Ser Gly Ala Phe
 85 90 95

Gln Leu Cys Gly Lys Val Phe Lys Ser Gly Glu Thr Thr Tyr Ser Cys
 100 105 110

Arg Asp Cys Ala Ile Asp Pro Thr Cys Val Leu Cys Met Asp Cys Phe
 115 120 125

Gln Ser Ser Val His Lys Asn His Arg Tyr Lys Met His Thr Ser Thr
 130 135 140

Gly Gly Gly Phe Cys Asp Cys Gly Asp Thr Glu Ala Trp Lys Thr Gly
 145 150 155 160

Pro	Phe	Cys	Val	Asp	His	Glu	Pro	Gly	Arg	Ala	Gly	Thr	Thr	Lys	Glu	165	170	175
Ser	Leu	His	Cys	Pro	Leu	Asn	Glu	Glu	Val	Ile	Ala	Gln	Ala	Arg	Arg	180	185	190
Ile	Phe	Pro	Ser	Val	Ile	Lys	Tyr	Ile	Val	Glu	Met	Thr	Ile	Trp	Glu	195	200	205
Glu	Glu	Lys	Glu	Leu	Pro	Pro	Glu	Leu	Gln	Ile	Arg	Glu	Lys	Asn	Glu	210	215	220
Arg	Tyr	Tyr	Cys	Val	Leu	Phe	Asn	Asp	Glu	His	His	Ser	Tyr	Asp	His	225	230	235
Val	Ile	Tyr	Ser	Leu	Gln	Arg	Ala	Leu	Asp	Cys	Glu	Leu	Ala	Glu	Ala	245	250	255
Gln	Leu	His	Thr	Thr	Ala	Ile	Asp	Lys	Glu	Gly	Arg	Arg	Ala	Val	Lys	260	265	270
Ala	Gly	Val	Tyr	Ala	Thr	Cys	Gln	Glu	Ala	Lys	Glu	Asp	Ile	Lys	Ser	275	280	285
His	Ser	Glu	Asn	Val	Ser	Gln	His	Pro	Leu	His	Val	Glu	Val	Leu	His	290	295	300
Ser	Val	Val	Met	Ala	His	Gln	Lys	Phe	Ala	Leu	Arg	Leu	Gly	Ser	Trp	305	310	315
Met	Asn	Lys	Ile	Met	Ser	Tyr	Ser	Ser	Asp	Phe	Arg	Gln	Ile	Phe	Cys	325	330	335
Gln	Ala	Cys	Leu	Val	Glu	Glu	Pro	Gly	Ser	Glu	Asn	Pro	Cys	Leu	Ile	340	345	350
Ser	Arg	Leu	Met	Leu	Trp	Asp	Ala	Lys	Leu	Tyr	Lys	Gly	Ala	Arg	Lys	355	360	365
Ile	Leu	His	Glu	Leu	Ile	Phe	Ser	Ser	Phe	Phe	Met	Glu	Met	Glu	Tyr	370	375	380
Lys	Lys	Leu	Phe	Ala	Met	Glu	Phe	Val	Lys	Tyr	Tyr	Lys	Gln	Leu	Gln	385	390	395
Lys	Glu	Tyr	Ile	Ser	Asp	Asp	His	Glu	Arg	Ser	Ile	Ser	Ile	Thr	Ala	405	410	415
Leu	Ser	Val	Gln	Met	Leu	Thr	Val	Pro	Thr	Leu	Ala	Arg	His	Leu	Ile	420	425	430
Glu	Glu	Gln	Asn	Val	Ile	Ser	Val	Ile	Thr	Glu	Thr	Leu	Leu	Glu	Val	435	440	445
Leu	Pro	Glu	Tyr	Leu	Asp	Arg	Asn	Asn	Lys	Phe	Asn	Phe	Gln	Gly	Tyr	450	455	460
Ser	Gln	Asp	Lys	Leu	Gly	Arg	Val	Tyr	Ala	Val	Ile	Cys	Asp	Leu	Lys	465	470	475
Tyr	Ile	Leu	Ile	Ser	Lys	Pro	Val	Ile	Trp	Thr	Glu	Arg	Leu	Arg	Ala	485	490	495

Gln Phe Leu Glu Gly Phe Arg Ser Phe Leu Lys Ile Leu Thr Cys Met
 500 505 510
 Gln Gly Met Glu Glu Ile Arg Arg Gln Val Gly Gln His Ile Glu Val
 515 520 525
 Asp Pro Asp Trp Glu Ala Ala Ile Ala Ile Gln Met Gln Leu Lys Asn
 530 535 540
 Ile Leu Leu Met Phe Gln Glu Trp Cys Ala Cys Asp Glu Asp Leu Leu
 545 550 555 560
 Leu Val Ala Tyr Lys Glu Cys His Lys Ala Val Met Arg Cys Ser Thr
 565 570 575
 Asn Phe Met Ser Ser Thr Lys Thr Val Val Gln Leu Cys Gly His Ser
 580 585 590
 Leu Glu Thr Lys Ser Tyr Lys Val Ser Glu Asp Leu Val Ser Ile His
 595 600 605
 Leu Pro Leu Ser Arg Thr Leu Ala Gly Leu His Val Arg Leu Ser Arg
 610 615 620
 Leu Gly Ala Ile Ser Arg Leu His Glu Phe Val Pro Phe Asp Ser Phe
 625 630 635 640
 Gln Val Glu Val Leu Val Glu Tyr Pro Leu Arg Cys Leu Val Leu Val
 645 650 655
 Ala Gln Val Val Ala Glu Met Trp Arg Arg Asn Gly Leu Ser Leu Ile
 660 665 670
 Ser Gln Val Phe Tyr Tyr Gln Asp Val Lys Cys Arg Glu Glu Met Tyr
 675 680 685
 Asp Lys Asp Ile Ile Met Leu Gln Ile Gly Ala Ser Ile Met Asp Pro
 690 695 700
 Asn Lys Phe Leu Leu Leu Val Leu Gln Arg Tyr Glu Leu Thr Asp Ala
 705 710 715 720
 Phe Asn Lys Thr Ile Ser Thr Lys Asp Gln Asp Leu Ile Lys Gln Tyr
 725 730 735
 Asn Thr Leu Ile Glu Glu Met Leu Gln Val Leu Ile Tyr Ile Val Gly
 740 745 750
 Glu Arg Tyr Val Pro Gly Val Gly Asn Val Thr Arg Glu Glu Val Ile
 755 760 765
 Met Arg Glu Ile Thr His Leu Leu Cys Ile Glu Pro Met Pro His Ser
 770 775 780
 Ala Ile Ala Arg Asn Leu Pro Glu Asn Glu Asn Asn Glu Thr Gly Leu
 785 790 795 800
 Glu Asn Val Ile Asn Lys Val Ala Thr Phe Lys Lys Pro Gly Val Ser
 805 810 815
 Gly His Gly Val Tyr Glu Leu Lys Asp Glu Ser Leu Lys Asp Phe Asn
 820 825 830

Met Tyr Phe Tyr His Tyr Ser Lys Thr Gln His Ser Lys Ala Glu His
 835 840 845
 Met Gln Lys Lys Arg Arg Lys Gln Glu Asn Lys Asp Glu Ala Leu Pro
 850 855 860
 Pro Pro Pro Pro Pro Glu Phe Cys Pro Ala Phe Ser Lys Val Val Asn
 865 870 875 880
 Leu Leu Ser Cys Asp Val Met Ile Tyr Ile Leu Arg Thr Ile Phe Glu
 885 890 895
 Arg Ala Val Asp Thr Glu Ser Asn Leu Trp Thr Glu Gly Met Leu Gln
 900 905 910
 Met Ala Phe His Ile Leu Ala Leu Gly Leu Leu Glu Glu Lys Gln Gln
 915 920 925
 Leu Gln Lys Ala Pro Glu Glu Glu Val Ala Phe Asp Phe Tyr His Lys
 930 935 940
 Ala Ser Arg Leu Gly Ser Ser Ala Met Asn Ala Gln Asn Ile Gln Met
 945 950 955 960
 Leu Leu Glu Arg Leu Lys Gly Ile Pro Gln Leu Glu Gly Gln Lys Asp
 965 970 975
 Met Ile Thr Trp Ile Leu Gln Met Phe Asp Thr Val Lys Arg Leu Arg
 980 985 990
 Glu Lys Ser Cys Leu Val Val Ala Thr Thr Ser Gly Leu Glu Cys Ile
 995 1000 1005
 Lys Ser Glu Glu Ile Thr His Asp Lys Glu Lys Ala Glu Arg Lys
 1010 1015 1020
 Arg Lys Ala Glu Ala Ala Arg Leu His Arg Gln Lys Ile Met Ala
 1025 1030 1035
 Gln Met Ser Ala Leu Gln Lys Asn Phe Ile Glu Thr His Lys Leu
 1040 1045 1050
 Met Tyr Asp Asn Thr Ser Glu Val Thr Gly Lys Glu Asp Ser Ile
 1055 1060 1065
 Met Glu Glu Glu Ser Thr Ser Ala Val Ser Glu Ala Ser Arg Ile
 1070 1075 1080
 Ala Leu Gly Pro Lys Arg Gly Pro Ala Val Thr Glu Lys Glu Val
 1085 1090 1095
 Leu Thr Cys Ile Leu Cys Gln Glu Glu Gln Glu Val Lys Leu Glu
 1100 1105 1110
 Asn Asn Ala Met Val Leu Ser Ala Cys Val Gln Lys Ser Thr Ala
 1115 1120 1125
 Leu Thr Gln His Arg Gly Lys Pro Val Asp His Leu Gly Glu Thr
 1130 1135 1140
 Leu Asp Pro Leu Phe Met Asp Pro Asp Leu Ala His Gly Thr Tyr
 1145 1150 1155

Thr	Gly	Ser	Cys	Gly	His	Val	Met	His	Ala	Val	Cys	Trp	Gln	Lys
1160						1165					1170			
Tyr	Phe	Glu	Ala	Val	Gln	Leu	Ser	Ser	Gln	Gln	Arg	Ile	His	Val
1175						1180					1185			
Asp	Leu	Phe	Asp	Leu	Glu	Ser	Gly	Glu	Tyr	Leu	Cys	Pro	Leu	Cys
1190						1195					1200			
Lys	Ser	Leu	Cys	Asn	Thr	Val	Ile	Pro	Ile	Ile	Pro	Leu	Gln	Pro
1205						1210					1215			
Gln	Lys	Ile	Asn	Ser	Glu	Asn	Ala	Glu	Ala	Leu	Ala	Gln	Leu	Leu
1220						1225					1230			
Thr	Leu	Ala	Arg	Trp	Ile	Gln	Thr	Val	Leu	Ala	Arg	Ile	Ser	Gly
1235						1240					1245			
Tyr	Asn	Ile	Lys	His	Ala	Lys	Gly	Glu	Ala	Pro	Ala	Val	Pro	Val
1250						1255					1260			
Leu	Phe	Asn	Gln	Gly	Met	Gly	Asp	Ser	Thr	Phe	Glu	Phe	His	Ser
1265						1270					1275			
Ile	Leu	Ser	Phe	Gly	Val	Gln	Ser	Ser	Val	Lys	Tyr	Ser	Asn	Ser
1280						1285					1290			
Ile	Lys	Glu	Met	Val	Ile	Leu	Phe	Ala	Thr	Thr	Ile	Tyr	Arg	Ile
1295						1300					1305			
Gly	Leu	Lys	Val	Pro	Pro	Asp	Glu	Leu	Asp	Pro	Arg	Val	Pro	Met
1310						1315					1320			
Met	Thr	Trp	Ser	Thr	Cys	Ala	Phe	Thr	Ile	Gln	Ala	Ile	Glu	Asn
1325						1330					1335			
Leu	Leu	Gly	Asp	Glu	Gly	Lys	Pro	Leu	Phe	Gly	Ala	Leu	Gln	Asn
1340						1345					1350			
Arg	Gln	His	Ser	Gly	Leu	Lys	Ala	Leu	Met	Gln	Phe	Ala	Val	Ala
1355						1360					1365			
Gln	Arg	Ala	Thr	Cys	Pro	Gln	Val	Leu	Ile	His	Lys	His	Leu	Ala
1370						1375					1380			
Arg	Leu	Leu	Ser	Val	Ile	Leu	Pro	Asn	Leu	Gln	Ser	Glu	Asn	Thr
1385						1390					1395			
Pro	Gly	Leu	Leu	Ser	Val	Asp	Leu	Phe	His	Val	Leu	Val	Gly	Ala
1400						1405					1410			
Val	Leu	Ala	Phe	Pro	Ser	Leu	Tyr	Trp	Asp	Asp	Thr	Val	Asp	Leu
1415						1420					1425			
Gln	Pro	Ser	Pro	Leu	Ser	Ser	Ser	Tyr	Asn	His	Leu	Tyr	Leu	Phe
1430						1435					1440			
His	Leu	Ile	Thr	Met	Ala	His	Met	Leu	Gln	Ile	Leu	Leu	Thr	Thr
1445						1450					1455			
Asp	Thr	Asp	Leu	Ser	Pro	Gly	Pro	Pro	Leu	Ala	Glu	Gly	Glu	Glu
1460						1465					1470			

Asp	Ser	Glu	Glu	Ala	Arg	Cys	Ala	Ser	Ala	Phe	Phe	Val	Glu	Val
1475						1480					1485			
Ser	Gln	His	Thr	Asp	Gly	Leu	Thr	Gly	Cys	Gly	Ala	Pro	Gly	Trp
1490						1495					1500			
Tyr	Leu	Trp	Leu	Ser	Leu	Arg	Asn	Gly	Ile	Thr	Pro	Tyr	Leu	Arg
1505						1510					1515			
Cys	Ala	Ala	Leu	Leu	Phe	His	Tyr	Leu	Leu	Gly	Val	Ala	Pro	Pro
1520						1525					1530			
Glu	Glu	Leu	Phe	Ala	Asn	Ser	Ala	Glu	Gly	Glu	Phe	Ser	Ala	Leu
1535						1540					1545			
Cys	Ser	Tyr	Leu	Ser	Leu	Pro	Thr	Asn	Leu	Phe	Leu	Leu	Phe	Gln
1550						1555					1560			
Glu	Tyr	Trp	Asp	Thr	Ile	Arg	Pro	Leu	Leu	Gln	Arg	Trp	Cys	Gly
1565						1570					1575			
Asp	Pro	Ala	Leu	Leu	Lys	Ser	Leu	Lys	Gln	Lys	Ser	Ala	Val	Val
1580						1585					1590			
Arg	Tyr	Pro	Arg	Lys	Arg	Asn	Ser	Leu	Ile	Glu	Leu	Pro	Glu	Asp
1595						1600					1605			
Tyr	Ser	Cys	Leu	Leu	Asn	Gln	Ala	Ser	His	Phe	Arg	Cys	Pro	Arg
1610						1615					1620			
Ser	Ala	Asp	Asp	Glu	Arg	Lys	His	Pro	Val	Leu	Cys	Leu	Phe	Cys
1625						1630					1635			
Gly	Ala	Ile	Leu	Cys	Ser	Gln	Asn	Ile	Cys	Cys	Gln	Glu	Ile	Val
1640						1645					1650			
Asn	Gly	Glu	Glu	Val	Gly	Ala	Cys	Val	Phe	His	Ala	Leu	His	Cys
1655						1660					1665			
Gly	Ala	Gly	Val	Cys	Ile	Phe	Leu	Lys	Ile	Arg	Glu	Cys	Arg	Val
1670						1675					1680			
Val	Leu	Val	Glu	Gly	Lys	Ala	Arg	Gly	Cys	Ala	Tyr	Pro	Ala	Pro
1685						1690					1695			
Tyr	Leu	Asp	Glu	Tyr	Gly	Glu	Thr	Asp	Pro	Gly	Leu	Lys	Arg	Gly
1700						1705					1710			
Asn	Pro	Leu	His	Leu	Ser	Arg	Glu	Arg	Tyr	Arg	Lys	Leu	His	Leu
1715						1720					1725			
Val	Trp	Gln	Gln	His	Cys	Ile	Ile	Glu	Glu	Ile	Ala	Arg	Ser	Gln
1730						1735					1740			
Glu	Thr	Asn	Gln	Met	Leu	Phe	Gly	Phe	Asn	Trp	Gln	Leu	Leu	
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 <212> PRT
 <213> Artificial sequence

155

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<220>
<223> Description of Artificial Sequence: peptide

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<210> 17
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 17

Gly Gly Gly Gly Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
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<210> 18
<211> 5205
<212> DNA
<213> Homo sapiens

<220>
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<222> (662)
<223> n = A or T or G or C

<220>
<221> misc_feature
<222> (668)
<223> n = A or T or G or C

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catcatttgg cacaattggt gccagaaatt tactttgctg aaatggaccc agacttggaa 180
aagcaggagg aaagtgtaca aatgtcaata ttcactccac tggaatggta cttatttggg 240
gaagatccag atatttgctt agagaaattg aagcacagtg gagcatttca gctttgtggg 300
agggttttca aaagtggaga gacaacctat tcttgcaggg attgtgcaat tgatccaaca 360
tgtgtactct gtatggactg cttccaggac agtgttcata aaaatcatcg ttacaagatg 420
catacttcta ctggaggagg gttctgtgac tgtggagaca cagaggcatg gaaaactggc 480
cctttttgtg taaatcatga acctggaaga gcaggtacta taaaagagaa ttcacgctgt 540
ccgttgaatg aagaggtaat tgtccaagcc aggaaaatat ttccttcagt gataaaatat 600
gtcgtagaaa tgactatatg ggaagaggaa aaagaactgc ctctgaact ccagataagg 660
knryycvndh hsydhgtcat atacagccta caaagagctc ttgactgtga gctcgcagag 720
gccagttgc ataccactgc cattgacaaa gagggtcgtc gggctgttaa agcgggagct 780

156

A

tatgctgctt gccaggaagc aaaggaagat ataaagagtc attcagaaaa tgtctctcaa	840
catccacttc atgtagaagt attacactca gagattatgg ctcatcagaa atttgctttg	900
cgtcttggtt cctggatgaa caaaattatg agctattcaa gtgacttttag gcagatcttt	960
tgccaagcat gccttagaga agaacctgac tgggagaatc cctgtctcat aagcagggtta	1020
atgctttggg atgcaaagct ttataaaggt gcccgtaaga tccttcatga attgatcttc	1080
agcagttttt ttatggagat ggaatacaaa aaactctttg ctatggaatt tgtgaagtat	1140
tataaacaac tgcagaaaga atatatcagt gatgatcatg acagaagtat ctctataact	1200
gcactttcag ttcagatgtt tactgttcct actctggctc gacatcttat tgaagagcag	1260
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 <212> PRT
 <213> Homo sapiens

<400> 19

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Trp	Trp	Asp	Gln	Gln	Val	Asp	Phe	Tyr	Thr	Ala	Phe	Leu	His	His	Leu
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Glu	Lys	Gln	Glu	Glu	Ser	Val	Gln	Met	Ser	Ile	Phe	Thr	Pro	Leu	Glu
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His	Ser	Gly	Ala	Phe	Gln	Leu	Cys	Gly	Arg	Val	Phe	Lys	Ser	Gly	Glu
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Thr	Thr	Tyr	Ser	Cys	Arg	Asp	Cys	Ala	Ile	Asp	Pro	Thr	Cys	Val	Leu
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Cys	Met	Asp	Cys	Phe	Gln	Asp	Ser	Val	His	Lys	Asn	His	Arg	Tyr	Lys
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Ala	Trp	Lys	Thr	Gly	Pro	Phe	Cys	Val	Asn	His	Glu	Pro	Gly	Arg	Ala
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His	Ser	Tyr	Asp	His	Val	Ile	Tyr	Ser	Leu	Gln	Arg	Ala	Leu	Asp	Cys			
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Glu	Asp	Ile	Lys	Ser	His	Ser	Glu	Asn	Val	Ser	Gln	His	Pro	Leu	His			
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Asn	Pro	Cys	Leu	Ile	Ser	Arg	Leu	Met	Leu	Trp	Asp	Ala	Lys	Leu	Tyr			
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Met	Glu	Met	Glu	Tyr	Lys	Lys	Leu	Phe	Ala	Met	Glu	Phe	Val	Lys	Tyr			
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Ile	Ser	Ile	Thr	Ala	Leu	Ser	Val	Gln	Met	Phe	Thr	Val	Pro	Thr	Leu			
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Ala	Arg	His	Leu	Ile	Glu	Glu	Gln	Asn	Val	Ile	Ser	Val	Ile	Thr	Glu			
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Gln His Ile Glu Val Asp Pro Asp Trp Glu Ala Ala Ile Ala Ile Gln
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 Met Gln Leu Lys Asn Ile Leu Leu Met Phe Gln Glu Trp Cys Ala Cys
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 Asp Glu Glu Leu Leu Leu Val Ala Tyr Lys Glu Cys His Lys Ala Val
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 Ser Cys Gly His Ser Leu Glu Thr Lys Ser Tyr Arg Val Ser Glu Asp
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 675 680 685
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 690 695 700
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 Ile Tyr Ile Val Gly Glu Arg Tyr Val Pro Gly Val Gly Asn Val Thr
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 Lys Glu Glu Val Thr Met Arg Glu Ile Ile His Leu Leu Cys Ile Glu
 770 775 780
 Pro Met Pro His Ser Ala Ile Ala Lys Asn Leu Pro Glu Asn Glu Asn
 785 790 795 800
 Asn Glu Thr Gly Leu Glu Asn Val Ile Asn Lys Val Ala Thr Phe Lys
 805 810 815
 Lys Pro Gly Val Ser Gly His Gly Val Tyr Glu Leu Lys Asp Glu Ser
 820 825 830
 Leu Lys Asp Phe Asn Met Tyr Phe Tyr His Tyr Ser Lys Thr Gln His
 835 840 845
 Ser Lys Ala Glu His Met Gln Lys Lys Arg Arg Lys Gln Glu Asn Lys
 850 855 860

Asp	Glu	Ala	Leu	Pro	Pro	Pro	Pro	Pro	Pro	Glu	Phe	Cys	Pro	Ala	Phe	865	870	875	880
Ser	Lys	Val	Ile	Asn	Leu	Leu	Asn	Cys	Asp	Ile	Met	Met	Tyr	Ile	Leu	885	890	895	
Arg	Thr	Val	Phe	Glu	Arg	Ala	Ile	Asp	Thr	Asp	Ser	Asn	Leu	Trp	Thr	900	905	910	
Glu	Gly	Met	Leu	Gln	Met	Ala	Phe	His	Ile	Leu	Ala	Leu	Gly	Leu	Leu	915	920	925	
Glu	Glu	Lys	Gln	Gln	Leu	Gln	Lys	Ala	Pro	Glu	Glu	Glu	Val	Thr	Phe	930	935	940	
Asp	Phe	Tyr	His	Lys	Ala	Ser	Arg	Leu	Gly	Ser	Ser	Ala	Met	Asn	Ile	945	950	955	960
Gln	Met	Leu	Leu	Glu	Lys	Leu	Lys	Gly	Ile	Pro	Gln	Leu	Glu	Gly	Gln	965	970	975	
Lys	Asp	Met	Ile	Thr	Trp	Ile	Leu	Gln	Met	Phe	Asp	Thr	Val	Lys	Arg	980	985	990	
Leu	Arg	Glu	Lys	Ser	Cys	Leu	Ile	Val	Ala	Thr	Thr	Ser	Gly	Ser	Glu	995	1000	1005	
Ser	Ile	Lys	Asn	Asp	Glu	Ile	Thr	His	Asp	Lys	Glu	Lys	Ala	Glu		1010	1015	1020	
Arg	Lys	Arg	Lys	Ala	Glu	Ala	Ala	Arg	Leu	His	Arg	Gln	Lys	Ile		1025	1030	1035	
Met	Ala	Gln	Met	Ser	Ala	Leu	Gln	Lys	Asn	Phe	Ile	Glu	Thr	His		1040	1045	1050	
Lys	Leu	Met	Tyr	Asp	Asn	Thr	Ser	Glu	Met	Pro	Gly	Lys	Glu	Asp		1055	1060	1065	
Ser	Ile	Met	Glu	Glu	Glu	Ser	Thr	Pro	Ala	Val	Ser	Asp	Tyr	Ser		1070	1075	1080	
Arg	Ile	Ala	Leu	Gly	Pro	Lys	Arg	Gly	Pro	Ser	Val	Thr	Glu	Lys		1085	1090	1095	
Glu	Val	Leu	Thr	Cys	Ile	Leu	Cys	Gln	Glu	Glu	Gln	Glu	Val	Lys		1100	1105	1110	
Ile	Glu	Asn	Asn	Ala	Met	Val	Leu	Ser	Ala	Cys	Val	Gln	Lys	Ser		1115	1120	1125	
Thr	Ala	Leu	Thr	Gln	His	Arg	Gly	Lys	Pro	Ile	Glu	Leu	Ser	Gly		1130	1135	1140	
Glu	Ala	Leu	Asp	Pro	Leu	Phe	Met	Asp	Pro	Asp	Leu	Ala	Tyr	Gly		1145	1150	1155	
Thr	Tyr	Thr	Gly	Ser	Cys	Gly	His	Val	Met	His	Ala	Val	Cys	Trp		1160	1165	1170	
Gln	Lys	Tyr	Phe	Glu	Ala	Val	Gln	Leu	Ser	Ser	Gln	Gln	Arg	Ile		1175	1180	1185	

His Val Asp Leu Phe Asp Leu Glu Ser Gly Glu Tyr Leu Cys Pro	1190	1195	1200
Leu Cys Lys Ser Leu Cys Asn Thr Val Ile Pro Ile Ile Pro Leu	1205	1210	1215
Gln Pro Gln Lys Ile Asn Ser Glu Asn Ala Asp Ala Leu Ala Gln	1220	1225	1230
Leu Leu Thr Leu Ala Arg Trp Ile Gln Thr Val Leu Ala Arg Ile	1235	1240	1245
Ser Gly Tyr Asn Ile Arg His Ala Lys Gly Glu Asn Pro Ile Pro	1250	1255	1260
Ile Phe Phe Asn Gln Gly Met Gly Asp Ser Thr Leu Glu Phe His	1265	1270	1275
Ser Ile Leu Ser Phe Gly Val Glu Ser Ser Ile Lys Tyr Ser Asn	1280	1285	1290
Ser Ile Lys Glu Met Val Ile Leu Phe Ala Thr Thr Ile Tyr Arg	1295	1300	1305
Ile Gly Leu Lys Val Pro Pro Asp Glu Arg Asp Pro Arg Val Pro	1310	1315	1320
Met Leu Thr Trp Ser Thr Cys Ala Phe Thr Ile Gln Ala Ile Glu	1325	1330	1335
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Asn Arg Gln His Asn Gly Leu Lys Ala Leu Met Gln Phe Ala Val	1355	1360	1365
Ala Gln Arg Ile Thr Cys Pro Gln Val Leu Ile Gln Lys His Leu	1370	1375	1380
Val Arg Leu Leu Ser Val Val Leu Pro Asn Ile Lys Ser Glu Asp	1385	1390	1395
Thr Pro Cys Leu Leu Ser Ile Asp Leu Phe His Val Leu Val Gly	1400	1405	1410
Ala Val Leu Ala Phe Pro Ser Leu Tyr Trp Asp Asp Pro Val Asp	1415	1420	1425
Leu Gln Pro Ser Ser Val Ser Ser Ser Tyr Asn His Leu Tyr Leu	1430	1435	1440
Phe His Leu Ile Thr Met Ala His Met Leu Gln Ile Leu Leu Thr	1445	1450	1455
Val Asp Thr Gly Leu Pro Leu Ala Gln Val Gln Glu Asp Ser Glu	1460	1465	1470
Glu Ala His Ser Ala Ser Ser Phe Phe Ala Glu Ile Ser Gln Tyr	1475	1480	1485
Thr Ser Gly Ser Ile Gly Cys Asp Ile Pro Gly Trp Tyr Leu Trp	1490	1495	1500

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Glu	Val	Gly	Ala	Cys	Ile	Phe	His	Ala	Leu	His	Cys	Lys	Ala	Arg
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Gly	Cys	Ala	Tyr	Pro	Ala	Pro	Tyr	Leu	Asp	Glu	Tyr	Gly	Glu	Thr
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1685						1690					1695			
Arg	Tyr	Arg	Lys	Leu	His	Leu	Val	Trp	Gln	Gln	His	Cys	Ile	Ile
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Glu	Glu	Ile	Ala	Arg	Ser	Gln	Glu	Thr	Asn	Gln	Met	Leu	Phe	Gly
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Phe	Asn	Trp	Gln	Leu	Leu									
1730														

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 <213> Artificial sequence

<220>
 <223> Description of Artificial Sequence: PCR Primer

<400> 20
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22

<210> 21
 <211> 20

<212> DNA
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 <220>
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 <210> 22
 <211> 18
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 <213> Artificial sequence

 <220>
 <223> Description of Artificial Sequence: PCR Primer

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 aggaagctgt gggtcatgt 18

 <210> 23
 <211> 14
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 <220>
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 <220>
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<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR Primer

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22

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<223> Description of Artificial Sequence: PCR Primer

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23

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21